(FILE 'HOME' ENTERED AT 14:23:31 ON 08 JAN 2007)

FILE 'REGISTRY' ENTERED AT 14:24:11 ON 08 JAN 2007 E "AMMONIAGENES"/CN 25 E "F0F1-ATPASE"/CN 25

FILE 'MEDLINE, AGRICOLA, CAPLUS, BIOSIS, EMBASE, WPIDS' ENTERED AT 14:25:07 ON 08 JAN 2007

L1 4 S AMMONIAGENES AND ATPASE

L2 3 DUP REM L1 (1 DUPLICATE REMOVED)

FILE 'STNGUIDE' ENTERED AT 14:26:38 ON 08 JAN 2007

L3 0 S AMMONIAGENES AND "PROTON PUMP"

FILE 'MEDLINE, AGRICOLA, CAPLUS, BIOSIS, EMBASE, WPIDS' ENTERED AT 14:49:42 ON 08 JAN 2007

L4 0 S AMMONIAGENES AND "PROTON PUMP"

L5 1954 S AMMONIAGENES

L6 2 S L5 AND F0F1?

L7 2 DUP REM L6 (0 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 14:50:45 ON 08 JAN 2007

L8 0 S L5 AND FOF1?

FILE 'REGISTRY' ENTERED AT 14:57:09 ON 08 JAN 2007

E "ATP SYNTHASE"/CN 25

L9 1 S E3

FILE 'MEDLINE, AGRICOLA, CAPLUS, BIOSIS, EMBASE, WPIDS' ENTERED AT 15:00:08 ON 08 JAN 2007

L10 10673 S L9

L11 0 S L5 AND L10

L12 0 S L5 AND 3.6.3.14

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Dec 18 2006 06:34:27

IUBMB Enzyme Nomenclature

EC 3.6.3.14

Accepted name: H⁺-transporting two-sector ATPase

Reaction: ATP + $H_2O + H_{in}^+ = ADP + phosphate + H_{out}^+$

Glossary: F_0 the "o" refers to oligomycin. F_0 is incorrect.

Other names: ATP synthase; F_1 -ATPase; F_0 -ATPase; F_0 -ATPase; F_0 -ATPase; mitochondrial ATPase; coupling factors (F_0 , F_1 and F_0); chloroplast ATPase; bacterial F_0 -ATPase

Systematic name: ATP phosphohydrolase (H⁺-transporting)

Comments: A multisubunit non-phosphorylated ATPase that is involved in the transport of ions. Large enzymes of mitochondria, chloroplasts and bacteria with a membrane sector (F_0, V_0, A_0) and a cytoplasmic-compartment sector (F_1, V_1, A_1) . The F-type enzymes of the inner mitochondrial and thylakoid membranes act as ATP synthases. All of the enzymes included here operate in a rotational mode, where the extramembrane sector (containing 3 α - and 3 β -subunits) is connected via the δ -subunit to the membrane sector by several smaller subunits. Within this complex, the γ - and ϵ -subunits, as well as the 9-12 c subunits rotate by consecutive 120° angles and perform parts of ATP synthesis. This movement is driven by the H⁺ electrochemical potential gradient. The V-type (in vacuoles and clathrincoated vesicles) and A-type (archebacterial) enzymes have a similar structure but, under physiological conditions, they pump H⁺ rather than synthesize ATP.

Links to other databases: BRENDA, EXPASY, KEGG, ERGO, PDB, CAS registry number:

References:

- 1. Boyer, P.D. The binding change mechanism for ATP synthase some probabilities and possibilities. *Biochim. Biophys. Acta* 1140 (1993) 215-250. [Medline UI: 93112640]
- 2. Abrahams, J.P., Leslie, A.G.W., Lutter, R. and Walker, J.F. Structure at 2.8 Å resolution of F₁-ATPase from bovine heart mitochondria. *Nature* 375 (1994) 621-628. [Medline UI: 94344236]
- 3. Blair, A., Ngo, L., Park, J., Paulsen, I.T. and Saier, M.H., Jr. Phylogenetic analyses of the homologous transmembrane channel-forming proteins of the F₀F₁-ATPases of bacteria, chloroplasts and mitochondria. *Microbiology* 142 (1996) 17-32. [Medline UI: 96146047]
- 4. Noji, H., Yasuda, R., Yoshida, M. and Kinosita, K., Jr. Direct observation of the rotation of F₁-ATPase. *Nature* 386 (1997) 299-302. [Medline UI: 97222141]

[EC 3.6.3.14 created 1984 as EC 3.6.1.34, transferred 2000 to EC 3.6.3.14]

Return to EC 3.6.3 home page

Return to EC 3.6 home page

Return to EC 3 home page

Return to Enzymes home page

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- F(0)F(1)-ATP Synthase
- ATPase, H(+)
- Proton-Translocating ATPase Complexes
- ATPase Complexes, Proton-Translocating
- Complexes, Proton-Translocating ATPase
- Proton Translocating ATPase Complexes
- H(+)-Transporting ATPase
- F1F0 ATPase Complex
- ATP Dependent Proton Translocase
- H+ ATPase
- ATPase, H+
- F0F1 ATPase
- F(1)F(0)-ATPase
- Proton-Translocating ATPase Complex
- ATPase Complex, Proton-Translocating
- Proton Translocating ATPase Complex
- H+ Transporting ATP Synthase
- H(+)-Transporting ATP Synthase
- Adenosine Triphosphatase Complex
- Complex, Adenosine Triphosphatase
- Triphosphatase Complex, Adenosine
- Proton-Translocating ATPase, F1 Sector
- Proton Translocating ATPase, F1 Sector
- F1-ATPase
- ATPase, F1
- F1 ATPase
- Adenosinetriphosphatase F1
- F-1-ATPase
- F 1 ATPase
- H(+)-Transporting ATP Synthase, Acyl-Phosphate-Linked
- Proton-Translocating ATPase, F0 Sector
- Proton Translocating ATPase, F0 Sector
- ATPase, F0
- F0 ATPase
- F-0-ATPase
- F 0 ATPase

Previous Indexing:

Adenosine Triphosphatase (1966-1982)

All MeSH Categories

Chemicals and Drugs Category
Enzymes and Coenzymes
Enzymes

Hydrolases

Acid Anhydride Hydrolases

Adenosine Triphosphatases

Proton-Translocating AT

Bacterial ProtonTranslocating ATPas

Chloroplast Proton-Translocating ATPas H(+)-K(+)-Exchangi **ATPase** Mitochondrial Protoi Translocating ATPas Vacuolar Proton-Translocating ATPas

All MeSH Categories Chemicals and Drugs Category Enzymes and Coenzymes

Enzymes

Transferases Phosphotransferases

Phosphotransferases (Phosphate

Acceptor)

ATP Synthetase Complexe

Proton-Translocati: **ATPases**

> **Bacterial Prote Translocating ATPases**

Chloroplast Pr **Translocating ATPases**

Mitochondrial

Proton-

Translocating

ATPases

Vacuolar Prote **Translocating**

ATPases

All MeSH Categories

Chemicals and Drugs Category

Amino Acids, Peptides, and Proteins

Proteins

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Membrane Transport Proteins

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ATPases

Bacteria

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